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SEQUENCE LISTING

<110> Bayer Yakuhin, Ltd.

<120> REGULATION OF HUMAN P2Y15 G PROTEIN-COUPLED RECEPTOR

<130> x

<160> 6

<170> PatentIn version 3.2

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<211> 1014

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1014)

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tat gca gct gct ttt gga aat tgc act gat gaa aac atc cca ctc aag	96
Tyr Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys	
20 25 30	
atg cac tac ctc cct gtt att tat ggc att atc ttc ctc gtg gga ttt	144
Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe	
35 40 45	
cca ggc aat gca gta gtg ata tcc act tac att ttc aaa atg aga cct	192
Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro	
50 55 60	
tgg aag agc agc acc atc att atg ctg aac ctg gcc tgc aca gat ctg	240
Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu	
65 70 75 80	
ctg tat ctg acc agc ctc ccc ttc ctg att cac tac tat gcc agt ggc	288
Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly	
85 90 95	
gaa aac tgg atc ttt gga gat ttc atg tgt aag ttt atc cgc ttc agc	336
Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser	
100 105 110	
ttc cat ttc aac ctg tat agc agc atc ctc ttc ctc acc tgt ttc agc	384
Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser	
115 120 125	
atc ttc cgc tac tgt gtg atc att cac cca atg agc tgc ttt tcc att	432
Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile	
130 135 140	
cac aaa act cga tgt gca gtt gta gcc tgt gct gtg gtg tgg atc att	480
His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile	
145 150 155 160	

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tca ctg gta gct gtc att ccg atg acc ttc ttg atc aca tca acc aac	528
Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn	
165 170 175	
agg acc aac aga tca gcc tgt ctc gac ctc acc agt tcg gat gaa ctc	576
Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu	
180 185 190	
aat act att aag tgg tac aac ctg att ttg act gca act act ttc tgc	624
Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys	
195 200 205	
ctc ccc ttg gtg ata gtg aca ctt tgc tat acc acg att atc cac act	672
Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr	
210 215 220	
ctg acc cat gga ctg caa act gac agc tgc ctt aag cag aaa gca cga	720
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225 230 235 240	
agg cta acc att ctg cta ctc ctt gca ttt tac gta tgt ttt tta ccc	768
Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro	
245 250 255	
ttc cat atc ttg agg gtc att cgg atc gaa tct cgc ctg ctt tca atc	816
Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile	
260 265 270	
agt tgt tcc att gag aat cag atc cat gaa gct tac atc gtt tct aga	864
Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr Ile Val Ser Arg	
275 280 285	
cca tta gct gct ctg aac acc ttt ggt aac ctg tta cta tat gtg gtg	912
Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val	
290 295 300	
gtc agc gac aac ttt cag cag gct gtc tgc tca aca gtg aga tgc aaa	960
Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys	
305 310 315 320	
gta agc ggg aac ctt gag caa gca aag aaa att agt tac tca aac aac	1008
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cct tga	1014
Pro	

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 <212> PRT
 <213> Homo sapiens

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Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys
20 25 30

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Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe
 35 40 45

Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro
 50 55 60

Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu
 65 70 75 80

Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
 85 90 95

Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser
 100 105 110

Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
 115 120 125

Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
 130 135 140

His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile
 145 150 155 160

Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn
 165 170 175

Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu
 180 185 190

Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
 195 200 205

Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr
 210 215 220

Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg
 225 230 235 240

Arg Leu Thr Ile Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro
 245 250 255

Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile
 260 265 270

Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr Ile Val Ser Arg
 275 280 285

- 4 -

Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
 290 295 300

Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys
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 tac cca agt gct ctg gga aac tgc acc gac gag caa atc tca ttc aag 96
 Tyr Pro Ser Ala Leu Gly Asn Cys Thr Asp Glu Gln Ile Ser Phe Lys
 20 25 30
 atg cag tac ctt ccc gtc atc tat agc atc atc ttc ctc gtg ggc ttc 144
 Met Gln Tyr Leu Pro Val Ile Tyr Ser Ile Ile Phe Leu Val Gly Phe
 35 40 45
 ccg ggg aac aca gtg gcc atc tcc atc tac att ttc aag atg cgg ccg 192
 Pro Gly Asn Thr Val Ala Ile Ser Ile Tyr Ile Phe Lys Met Arg Pro
 50 55 60
 tgg agg ggc agt aca gtc atc atg ctg aac ctg gcc ttg acg gac ttg 240
 Trp Arg Gly Ser Thr Val Ile Met Leu Asn Leu Ala Leu Thr Asp Leu
 65 70 75 80
 ctg tat ctg acc agc ctc ccg ttc ctc atc cat tac tat gcc agt ggt 288
 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
 85 90 95
 gaa aac tgg atc ttt gga gat ttc atg tgc aag ttc atc cgc ttc ggc 336
 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Gly
 100 105 110
 ttc cac ttc aac ctc tac agc agc att ctc ttc ctc acc tgc ttc agt 384
 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
 115 120 125
 ctc ttc cgt tac gtt gtg atc att cac ccg atg agc tgc ttt tct att 432
 Leu Phe Arg Tyr Val Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
 130 135 140

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cag aaa act cgc tgg gca gtg gta gct tgt gcc ggg gtg tgg gtc att 480
 Gln Lys Thr Arg Trp Ala Val Val Ala Cys Ala Gly Val Trp Val Ile
 145 150 155 160
 tct ttg gta gct gtc atg ccc atg act ttc ctg atc aca tca acc acc 528
 Ser Leu Val Ala Val Met Pro Met Thr Phe Leu Ile Thr Ser Thr Thr
 165 170 175
 cgg acc aat agg tct gct tgc ctt gac ctc acc agt tca gat gac ctc 576
 Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Asp Leu
 180 185 190
 act act atc aag tgg tac aat ctc att ttg aca gcc acc act ttc tgc 624
 Thr Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Phe Cys
 195 200 205
 ctg cca ttg gtg ata gtg aca ctt tgc tac acg aca att atc agt acc 672
 Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile Ser Thr
 210 215 220
 ctg act cac ggg cct cgg acc cac agc tgc ttt aag cag aag gct cgg 720
 Leu Thr His Gly Pro Arg Thr His Ser Cys Phe Lys Gln Lys Ala Arg
 225 230 235 240
 aga ctg act att ctg ctc ctc ctt gtt ttc tat ata tgt ttc tta ccc 768
 Arg Leu Thr Ile Leu Leu Leu Leu Val Phe Tyr Ile Cys Phe Leu Pro
 245 250 255
 ttc cac atc ttg agg gtc att cgg atc gaa tct cgc ctg ctt tca atc 816
 Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile
 260 265 270
 agc tgc tcc atc gag agt cac atc cac gaa gct tac att gtt tct aga 864
 Ser Cys Ser Ile Glu Ser His Ile His Glu Ala Tyr Ile Val Ser Arg
 275 280 285
 cca tta gct gct ctc aac acc ttt ggc aac ctg ctg tta tat gtt gtg 912
 Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
 290 295 300
 gtc agc aat aac ttc cag cag gca ttc tgc tct ata gtg aga tgc aaa 960
 Val Ser Asn Asn Phe Gln Gln Ala Phe Cys Ser Ile Val Arg Cys Lys
 305 310 315 320
 gcc agt ggg gac ctt gaa caa gga aag aaa gac agt tgc tca aac aac 1008
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 325 330 335
 cct tga 1014
 Pro

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 <212> PRT
 <213> Mus musculus

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Tyr Pro Ser Ala Leu Gly Asn Cys Thr Asp Glu Gln Ile Ser Phe Lys
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Met Gln Tyr Leu Pro Val Ile Tyr Ser Ile Ile Phe Leu Val Gly Phe
 35 40 45

Pro Gly Asn Thr Val Ala Ile Ser Ile Tyr Ile Phe Lys Met Arg Pro
 50 55 60

Trp Arg Gly Ser Thr Val Ile Met Leu Asn Leu Ala Leu Thr Asp Leu
 65 70 75 80

Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
 85 90 95

Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Gly
 100 105 110

Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
 115 120 125

Leu Phe Arg Tyr Val Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
 130 135 140

Gln Lys Thr Arg Trp Ala Val Val Ala Cys Ala Gly Val Trp Val Ile
 145 150 155 160

Ser Leu Val Ala Val Met Pro Met Thr Phe Leu Ile Thr Ser Thr Thr
 165 170 175

Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Asp Leu
 180 185 190

Thr Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
 195 200 205

Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile Ser Thr
 210 215 220

Leu Thr His Gly Pro Arg Thr His Ser Cys Phe Lys Gln Lys Ala Arg
 225 230 235 240

Arg Leu Thr Ile Leu Leu Leu Val Phe Tyr Ile Cys Phe Leu Pro
 245 250 255

Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile
 260 265 270

- 7 -

Ser Cys Ser Ile Glu Ser His Ile His Glu Ala Tyr Ile Val Ser Arg
 275 280 285

Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
 290 295 300

Val Ser Asn Asn Phe Gln Gln Ala Phe Cys Ser Ile Val Arg Cys Lys
 305 310 315 320

Ala Ser Gly Asp Leu Glu Gln Gly Lys Lys Asp Ser Cys Ser Asn Asn
 325 330 335

Pro

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 Tyr Ile Thr Ala Leu Glu Asn Cys Thr Asp Glu Gln Ile Ser Phe Lys
 20 25 30
 atg cag tac ctt ccc gtc atc tac agc atc atc ttt ctc gtg ggc ttc 144
 Met Gln Tyr Leu Pro Val Ile Tyr Ser Ile Ile Phe Leu Val Gly Phe
 35 40 45
 ccg gga aat acg gtg gcg att tcc atc tac gtt ttc aag atg cga cct 192
 Pro Gly Asn Thr Val Ala Ile Ser Ile Tyr Val Phe Lys Met Arg Pro
 50 55 60
 tgg aag agc agt acc atc atc atg ctg aac ctg gcc ttg acg gac ttg 240
 Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Leu Thr Asp Leu
 65 70 75 80
 ctg tat ctg acc agc ctc cct ttc ctc atc cat tat tac gcg agc ggt 288
 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
 85 90 95
 gaa aac tgg atc ttc ggg gat ttc atg tgc aag ttc atc cga ttt ggc 336
 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Gly
 100 105 110
 ttc cat ttc aac ctt tac agc agc atc ctc ttc ctc acc tgc ttt agc 384
 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
 115 120 125

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cag aag act cga tgg gcg gtg gtg gct tgt gct ggg gtg tgg gtc att Gln Lys Thr Arg Trp Ala Val Val Ala Cys Ala Gly Val Trp Val Ile 145 150 155 160	480
tct ttg gta gct gtc atg ccc atg act ttc ctg atc aca tca acc acc Ser Leu Val Ala Val Met Pro Met Thr Phe Leu Ile Thr Ser Thr Thr 165 170 175	528
cgg acc aat agg tct gct tgc ctt gac ctc acc agc tca gat gac ctc Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Asp Leu 180 185 190	576
act act atc aaa tgg tac aat ctc att ttg acg gct acc act ttc tgc Thr Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys 195 200 205	624
ctg ccc ttg ctg ata gtg aca ctc tgc tac acg acg att atc agc acc Leu Pro Leu Leu Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile Ser Thr 210 215 220	672
ctg act cac gga cct cgg acc cac agc tgc ttt aag cag aag gct cgg Leu Thr His Gly Pro Arg Thr His Ser Cys Phe Lys Gln Lys Ala Arg 225 230 235 240	720
agg ctg acg atc ctg ctc ctc ctt gtg ttc tat gta tgc ttt tta ccc Arg Leu Thr Ile Leu Leu Leu Val Phe Tyr Val Cys Phe Leu Pro 245 250 255	768
ttc cac atc ctt agg gtc att cgg atc gaa tct cgc ctg ctt tca atc Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile 260 265 270	816
agc tgc tcc atc gag agt cac atc cac gaa gct tac att gtc tct agg Ser Cys Ser Ile Glu Ser His Ile His Glu Ala Tyr Ile Val Ser Arg 275 280 285	864
cca tta gct gcc ctc aac acc ttt ggc aac ctg ctg tta tat gtc gtc Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val 290 295 300	912
gtc agc aat aac ttc cag cag gca ttc tgc tcc gca gtg aga tgt aaa Val Ser Asn Asn Phe Gln Gln Ala Phe Cys Ser Ala Val Arg Cys Lys 305 310 315 320	960
gcc atc ggg gac ctt gaa caa gca aag aaa gac agt tgc tca aac aac Ala Ile Gly Asp Leu Glu Gln Ala Lys Lys Asp Ser Cys Ser Asn Asn 325 330 335	1008
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Met Gln Tyr Leu Pro Val Ile Tyr Ser Ile Ile Phe Leu Val Gly Phe
 35 40 45

Pro Gly Asn Thr Val Ala Ile Ser Ile Tyr Val Phe Lys Met Arg Pro
 50 55 60

Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Leu Thr Asp Leu
 65 70 75 80

Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
 85 90 95

Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Gly
 100 105 110

Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
 115 120 125

Leu Phe Arg Tyr Ile Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
 130 135 140

Gln Lys Thr Arg Trp Ala Val Val Ala Cys Ala Gly Val Trp Val Ile
 145 150 155 160

Ser Leu Val Ala Val Met Pro Met Thr Phe Leu Ile Thr Ser Thr Thr
 165 170 175

Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Asp Leu
 180 185 190

Thr Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
 195 200 205

Leu Pro Leu Leu Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile Ser Thr
 210 215 220

Leu Thr His Gly Pro Arg Thr His Ser Cys Phe Lys Gln Lys Ala Arg
 225 230 235 240

Arg Leu Thr Ile Leu Leu Leu Val Phe Tyr Val Cys Phe Leu Pro
 245 250 255

- 10 -

Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile
260 265 270

Ser Cys Ser Ile Glu Ser His Ile His Glu Ala Tyr Ile Val Ser Arg
275 280 285

Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
290 295 300

Val Ser Asn Asn Phe Gln Gln Ala Phe Cys Ser Ala Val Arg Cys Lys
305 310 315 320

Ala Ile Gly Asp Leu Glu Gln Ala Lys Lys Asp Ser Cys Ser Asn Asn
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Pro

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